

## AMENDMENTS TO THE SPECIFICATION

Amend the paragraph beginning at page 7, line 3, as follows:

Nucleic acid sequence identity can be determined in the following manner. The subject polynucleotide molecule sequence is used to search a nucleic acid sequence database, such as the Genbank database (~~accessible at Website <http://www.ncbi.nlm.nih.gov/blast/>~~), using the program BLASTN version 2.1 (based on Altschul et al., *Nucleic Acids Research* 25: 3389-3402 (1997)). The program is used in the ungapped mode. Default filtering is used to remove sequence homologies due to regions of low complexity as defined in Wootton, J.C. and S. Federhen, *Methods in Enzymology* 266: 554-571 (1996). The default parameters of BLASTN are utilized.

Amend the paragraph beginning at page 7, line 18, as follows:

Amino acid sequence identity can be determined in the following manner. The subject protein sequence is used to search a protein sequence database, such as the GenBank database (~~accessible at web site <http://www.ncbi.nlm.nih.gov/blast/>~~), using the BLASTP program. The program is used in the ungapped mode. Default filtering is used to remove sequence homologies due to regions of low complexity. The default parameters of BLASTP are utilized. Filtering for sequences of low complexity utilize the SEG program.